BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using BLAST engine for local alignment.
The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from NCBI ftp site
Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program [blastp |↕] Matrix [BLOSUM62 |↕]

Parameters used in BLASTN program only:
Reward for a match:[   ] **Penalty for a mismatch:**[   ]
☒ Use Mega BLAST   Strand option [Not Applicable |↕]

Open gap [11] and extension gap [1   ] penalties
gap x_dropoff [50] expect [10] word size [3   ] Filter ☑

Sequence 1 Enter accession or GI [l.r~G- P] or download from file [   ]

or sequence in FASTA format from:[   ] to:[   ]

```
gyvvtnnnvvanatvikvqisagrkraakmvgkaprsalailqiqnpknitaikmaasaal
rvgdytvaignpfglgetvtsgivsalgrsglnaenyenfiqtdaainrgnsggalvnlng
eligintailapdggnigigfaipsnmvknltsqmveygqvkrgelgimgtelnselakam
kvdaqrgafvsqvlpnssaakagikagdvitslngkpissfaalraqvgtmpvgskltlgl
lrdgkqvnvnlelqqssqnqvdsssifngiegaemsnkgkdqgvvvnnvktgtpaaqiglk
kgdviiganqqavkniaelrkvldskpsvlalniqrgdstiyllmq
```

DEG P of Eredi;

Sequence 2 Enter accession or GI [Gilbert] or download from file [   ]

or sequence in FASTA format from:[   ] to:[   ]

```
mglkkacltvlclivfcfgifytfdrvnhgernavsllkdklfneegepvnlifcytilqm
kvaerimaqhpgerfyvvlmsenrnekydyyfkqikdkaerayffhlpyglnksfnfiptm
aelkvksmllpkvkriylaslekvsiaaflstypdaeiktfddgtgnliqsssylgdefsv
ngtikrnfarmmigdwsiaktrnasdehytifkglknimddgrrkmtylplfdaselkagd
etggtvrillgspdkemkeisekaaknfniqyvaphprqtyglsgvttlnspyviedyilr
eikknphtryeiytffsgaaltmkdf
```

Gilbert
 # SEQ ID NO: 2

[Align] [Clear Input]

Comments and suggestions to: blast-help@ncbi.nlm.nih.gov
Credits to: Tatiana Tatusov *and* Tom Madden

Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.1 [Aug-1-2001]

Matrix [BLOSUM62 ◆] gap open: [11] gap extension: [1]

x_dropoff: [50] expect: [10.0] wordsize: [3] Filter ☑ [Align]

Sequence 1 lcl|seq_1   **Length** 473

Sequence 2 lcl|seq_2   **Length** 331

No significant similarity was found